

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

(i) APPLICANT: Blackburn, Michael  
Church, William  
Gross, Mitchell  
Feuerstein, Giora  
Nichols, Andrew  
Padlan, Eduardo  
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Sylvester, Daniel

(ii) TITLE OF THE INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
OF THROMBOSIS

(iii) NUMBER OF SEQUENCES: 111

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation  
(B) STREET: 709 Swedeland Road  
(C) CITY: King of Prussia  
(D) STATE: PA  
(E) COUNTRY: USA  
(F) ZIP: 19406

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ Version 1.5

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 16-JAN-1997  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/029,119  
(B) FILING DATE: 24-OCT-1996

## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Baumeister, Kirk
- (B) REGISTRATION NUMBER: 33,833
- (C) REFERENCE/DOCKET NUMBER: P50438

## (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-270-5096
- (B) TELEFAX:
- (C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CATCCTAGAG TCACCGAGGA

20

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGCTGCCCAA AGTGCCCAAG C

21

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTAACACTCA TTCCTGTTGA AGCTCTTGAC AATGGG

36

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATTTTCARG TGCAGATTTT C

21

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| CAGATCCAGT | TGGTGCAGTC | TGGACCTGAG | CTGAAGAAGC | CTGGAGAGAC  | AGTCAAGATC | 60  |
| TCCTGCAAGG | CTTCTGGGTA | CACCTTCACA | AACTATGGAA | TGAACTGGGT  | GAAGCAGGCT | 120 |
| CCAGGAAAGG | GTTTAAAGTG | GATGGGCTGG | ATAAACACCA | GAAATGGAAA  | GTCAACATAT | 180 |
| GTTGATGACT | TCAAGGGACG | GTTTGCCTTC | TCTTTGGAAA | GCTCTGCCAG  | CACTGCCAAT | 240 |
| TTGCAGATCG | ACAACCTCAA | AGATGAGGAC | ACGGCTACAT | ATTTCTGTAC  | AAGAGAAGGG | 300 |
| AATATGGATG | GTTACTTCCC | TTTTACTTAC | TGGGGCCAAG | GGA CTCTGGT | CACTGTCTCT | 360 |
| GCA        |            |            |            |             |            | 363 |

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

CAAATTGTTC TCTCCCAGTC TCCAGCAATC CTGTCTGCAT CTCCAGGGGA GAAGGTCACA    60
ATGACTTGCA GGGCCAGCTC AAGTGTAAT TACATGCACT GGTACCAGCA GAAGCCAGGA    120
TCCTCCCCCA AACCTGGAT TTATGCCACA TCCAACCTGG CTTCTGGAGT CCCTGCTCGC    180
TTCAGTGGCA GTGGGTCTGG GACCTCTTAC TCTCTCACAA TCAGCAGAGT GGAGGCTGAA    240
GATGCTGCCA CTTATTACTG CCAGCAGTGG AGTATTAACC CACGGACGTT CGGTGGAGGC    300
ACCAAGCTGG AAATCAAACG G                                     321

```

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE: internal

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1             5             10             15
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
      20             25             30
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
      35             40             45
Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe
      50             55             60
Lys Gly Arg Phe Ala Phe Ser Leu Glu Ser Ser Ala Ser Thr Ala Asn
      65             70             75             80
Leu Gln Ile Asp Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys
      85             90             95
Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly
      100            105            110
Gln Gly Thr Leu Val Thr Val Ser Ala
      115            120

```

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn Tyr Gly Met Asn

1 5

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys

1 5 10 15

Gly

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly  
 1                      5                      10                      15  
 Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met  
                     20                      25                      30  
 His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr  
                     35                      40                      45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser  
 50 55 60  
 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu  
 65 70 75 80  
 Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr  
 85 90 95  
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg  
 100 105

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Ala Ser Ser Ser Val Asn Tyr Met His  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Thr Ser Asn Leu Ala Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gln Gln Trp Ser Ile Asn Pro Arg Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|   |     |
|---|-----|
| CAACTAGTGC AATCTGGGTC TGAGTTGAAG AAGCCTGGGG CCTCAGTGAA GGTTTCCTGC | 60  |
| AAGGCCTCTG GATACACCTT CACTAACTAT GGAATGAACT GGGT                  | 104 |

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

TTGAAGTCAT CAACATATGT TGACTTTCCA TTTCTGGTGT TTATCCATCC CATCCACTCG      60
AGCCCTTGTC CAGGGGCCTG TCGCACCCAG TTCATTCCAT AGTTAGTG      108

```

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

GTCAACATAT GTTGATGACT TCAAGGGGCG GTTTGTCTTC CCTCTGTCAG CACGGCATAT      60
CTACAGATCA GCAGCCTAAA GGCTGACGAC ACTGCAGTGT ATTACTG      107

```

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|   |    |
|---|----|
| GGTACCCTGG CCCAGTAAG TAAAGGGAA GTAACCATCC ATATTCCTT CTCTGCACA | 60 |
| GTAATACACT GCAGTGTCTG CAGCCTTTAG G                            | 91 |

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 2...337
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| A   | CTA | GTG | CAA | TCT | GGG | TCT | GAG | TTG | AAG | AAG | CCT | GGG | GCC | TCA | GTG | AAG | 49 |
|     | Leu | Val | Gln | Ser | Gly | Ser | Glu | Leu | Lys | Lys | Pro | Gly | Ala | Ser | Val | Lys |    |
|     | 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |    |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| GTT | TCC | TGC | AAG | GCC | TCT | GGA | TAC | ACC | TTC | ACT | AAC | TAT | GGA | ATG | AAC | 97  |    |
| Val | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Thr | Asn | Tyr | Gly | Met | Asn |     |    |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |    |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| TGG | GTG | CGA | CAG | GCC | CCT | GGA | CAA | GGG | CTC | GAG | TGG | ATG | GGA | TGG | ATA | 145 |    |
| Trp | Val | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu | Glu | Trp | Met | Gly | Trp | Ile |     |    |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |    |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| AAC | ACC | AGA | AAT | GGA | AAG | TCA | ACA | TAT | GTT | GAT | GAC | TTC | AAG | GGG | CGG | 193 |    |
| Asn | Thr | Arg | Asn | Gly | Lys | Ser | Thr | Tyr | Val | Asp | Asp | Phe | Lys | Gly | Arg |     |    |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |    |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| TTT | GTC | TTC | TCC | TTG | GAC | ACC | TCT | GTC | AGC | ACG | GCA | TAT | CTA | CAG | ATC | 241 |    |
| Phe | Val | Phe | Ser | Leu | Asp | Thr | Ser | Val | Ser | Thr | Ala | Tyr | Leu | Gln | Ile |     |    |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |    |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| AGC | AGC | CTA | AAG | GCT | GAC | GAC | ACT | GCA | GTG | TAT | TAC | TGT | GCG | AGA | GAA | 289 |    |
| Ser | Ser | Leu | Lys | Ala | Asp | Asp | Thr | Ala | Val | Tyr | Tyr | Cys | Ala | Arg | Glu |     |    |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |    |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| GGG | AAT | ATG | GAT | GGT | TAC | TTC | CCT | TTT | ACT | TAC | TGG | GGC | CAG | GGT | ACC | 337 |    |
| Gly | Asn | Met | Asp | Gly | Tyr | Phe | Pro | Phe | Thr | Tyr | Trp | Gly | Gln | Gly | Thr |     |    |
|     |     |     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |    |

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Gln | Ser | Gly | Ser | Glu | Leu | Lys | Lys | Pro | Gly | Ala | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Thr | Asn | Tyr | Gly | Met | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Val | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu | Glu | Trp | Met | Gly | Trp | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Thr | Arg | Asn | Gly | Lys | Ser | Thr | Tyr | Val | Asp | Asp | Phe | Lys | Gly | Arg |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Phe | Val | Phe | Ser | Leu | Asp | Thr | Ser | Val | Ser | Thr | Ala | Tyr | Leu | Gln | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Ser | Leu | Lys | Ala | Asp | Asp | Thr | Ala | Val | Tyr | Tyr | Cys | Ala | Arg | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Gly | Asn | Met | Asp | Gly | Tyr | Phe | Pro | Phe | Thr | Tyr | Trp | Gly | Gln | Gly | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCTACTAGTG CAATCTGGGT CTGAGTTGAA GCC

33

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGGGTACCCT GGGCCAGTA AGTAAAAGGG

30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 27...95  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC  
 Met Gly Trp Ser Cys Ile Ile Leu Phe  
 1 5

53

TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG GTC CAA CTA GT  
 Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Val Gln Leu  
 10 15 20

97

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE: internal

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 1 5 10 15  
 Val His Ser Gln Val Gln Leu  
 20

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGAGACGCCA TCGAATTCTG AGCACACAGG ACCTCACCAT GGGATGGAGC TGTATCATCC 60  
TCTTCTTGGT AGCAACAGCT ACAGGTGTCC ACTCCCAGGT CCAACTGCAG 110

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGAGACGCCA TCGAATTCTG A 21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GATTGCACTA GTTGGACCTG GGAGTGGACA 30



## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAGAGTGGG TCGCAGAGAT CTCTGATGGT GGTAGTTACA CCTACTATCC AGACACTGTG 60  
ACGGGCCCGGT TCACGAT 77

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATCGTGAACC GGCCCGTCAC AGTGTCTGGA TAGTAGGTGT AACTACCACC ATCAGAGATC 60  
TCTGCGACCC ACT 73

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...363

(D) OTHER INFORMATION: F9HZHC 1-0

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

|   |     |
|---|-----|
| CAG GTG CAA CTA GTG CAA TCT GGG TCT GAG TTG AAG AAG CCT GGG GCC | 48  |
| Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala |     |
| 1 5 10 15   |     |
| TCA GTG AAG GTT TCC TGC AAG GCC TCT GGA TAC ACC TTC ACT AAC TAT | 96  |
| Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr |     |
| 20 25 30  |     |
| GGA ATG AAC TGG GTG CGA CAG GCC CCT GGA CAA GGG CTC GAG TGG ATG | 144 |
| Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met |     |
| 35 40 45  |     |
| GGA TGG ATA AAC ACC AGA AAT GGA AAG TCA ACA TAT GTT GAT GAC TTC | 192 |
| Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe |     |
| 50 55 60  |     |
| AAG GGA CGG TTT GTC TTC TCC TTG GAC ACC TCT GTC AGC ACG GCA TAT | 240 |
| Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr |     |
| 65 70 75 80   |     |

CTA CAG ATC AGC AGC CTA AAG GCT GAC GAC ACT GCA GTG TAT TAC TGT 288  
 Leu Gln Ile Ser Ser Leu Lys Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
                     85                    90                    95

GCG AGA GAA GGG AAT ATG GAT GGT TAC TTC CCT TTT ACT TAC TGG GGC 336  
 Ala Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly  
                     100                    105                    110

CAG GGT ACC CTG GTC ACC GTC TCC TCA 363  
 Gln Gly Thr Leu Val Thr Val Ser Ser  
                     115                    120

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala  
 1                    5                    10                    15  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr  
                     20                    25                    30  
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
                     35                    40                    45  
 Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe  
                     50                    55                    60  
 Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr  
 65                    70                    75                    80  
 Leu Gln Ile Ser Ser Leu Lys Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
                     85                    90                    95  
 Ala Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly  
                     100                    105                    110

Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

AGTACTGACA CAGTCTCCAG CCACCCTGTC TTTGTCTCCA GGGGAAAGAG CCACCCTCTC      60
CTGCAGGGCC AGCTCAAGTG TAAATTACAT GCACTGGTAC CAACAGAGAC CTGGCCAGGC      120
TCCCAGGCTC CTCATCTATG CCACTAGTAA CCTGGCTTCT GGCAT                      165

```

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

CCGCGGGTTA ATACTCCACT GCTGACAGTA ATAAACCGCA AAATCTTCAG GCTCTAGACT      60
GCTGATGGTG AGAGTGAAAT CTGTCCCAGA CCCGGATCCA CTGAACCTGG CTGGGATGCC      120
AGAAGCCAGG TTACTAGTGG CATAGA                      146

```

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 2...280

(D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| A   | GTA | CTG | ACA | CAG | TCT | CCA | GCC | ACC | CTG | TCT | TTG | TCT | CCA | GGG | GAA | AGA | 49  |
|     | Val | Leu | Thr | Gln | Ser | Pro | Ala | Thr | Leu | Ser | Leu | Ser | Pro | Gly | Glu | Arg |     |
|     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GCC | ACC | CTC | TCC | TGC | AGG | GCC | AGC | TCA | AGT | GTA | AAT | TAC | ATG | CAC | TGG |     | 97  |
| Ala | Thr | Leu | Ser | Cys | Arg | Ala | Ser | Ser | Ser | Val | Asn | Tyr | Met | His | Trp |     |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| TAC | CAA | CAG | AGA | CCT | GGC | CAG | GCT | CCC | AGG | CTC | CTC | ATC | TAT | GCC | ACT |     | 145 |
| Tyr | Gln | Gln | Arg | Pro | Gly | Gln | Ala | Pro | Arg | Leu | Leu | Ile | Tyr | Ala | Thr |     |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| AGT | AAC | CTG | GCT | TCT | GGC | ATC | CCA | GCC | AGG | TTC | AGT | GGA | TCC | GGG | TCT |     | 193 |
| Ser | Asn | Leu | Ala | Ser | Gly | Ile | Pro | Ala | Arg | Phe | Ser | Gly | Ser | Gly | Ser |     |     |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GGG | ACA | GAT | TTC | ACT | CTC | ACC | ATC | AGC | AGT | CTA | GAG | CCT | GAA | GAT | TTT |     | 241 |
| Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Glu | Pro | Glu | Asp | Phe |     |     |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |     |

GCG GTT TAT TAC TGT CAG CAG TGG AGT ATT AAC CCG CGG  
 Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg  
                   85                                  90

280

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE: internal

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg  
   1                  5                                  10                                  15  
 Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Asn Tyr Met His Trp  
                   20                                  25                                  30  
 Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ala Thr  
                   35                                  40                                  45  
 Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser  
                   50                                  55                                  60  
 Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe  
                   65                                  70                                  75                                  80  
 Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg  
                   85                                  90

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TCGAGTACTG ACACAGTCTC CAGCCAC

27

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GACCGCGGGT TAATACTCCA CTGCTGA

27

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 27...92  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC 53  
 Met Gly Trp Ser Cys Ile Ile Leu Phe  
 1 5

TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC GAG ATA GTA CT 94  
 Leu Val Ala Thr Ala Thr Gly Val His Ser Glu Ile Val  
 10 15 20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 1 5 10 15  
 Val His Ser Glu Ile Val  
 20

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid



- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GACTGTGTCA GTACTATCTC GGAGTGGACA

30

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGGCAGCCTC CTAAGTTGCT CATTTACTGG GCGTCGACTA GGGAATCTGG GGTAC

55

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCCAGATTCC CTAGTCGACG CCCAGTAAAT GAGCAACTTA GGAGGCTGCC C

51

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...321

(D) OTHER INFORMATION: F9HZLC1-0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAA ATA GTA CTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG 48  
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

GAA AGA GCC ACC CTC TCC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG 96  
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Asn Tyr Met  
20 25 30

CAC TGG TAC CAA CAG AGA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT 144  
His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr  
35 40 45

```

GCC ACT AGT AAC CTG GCT TCT GGC ATC CCA GCC AGG TTC AGT GGA TCC      192
Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
    50                      55                      60

GGG TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTA GAG CCT GAA      240
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
    65                      70                      75                      80

GAT TTT GCG GTT TAT TAC TGT CAG CAG TGG AGT ATT AAC CCG CGG ACG      288
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr
                      85                      90                      95

TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA                        321
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
    100                      105

```

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE: internal

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1              5              10              15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Asn Tyr Met
    20              25              30
His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
    35              40              45
Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
    50              55              60
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
    65              70              75              80

```

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr  
                             85                            90                            95  
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
                             100                            105

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

|   |     |
|---|-----|
| CCTGGACAAG GGCTCAAGTG GATGGGATGG ATAAACACCA GAAATGGAAA GTCAACATAT | 60  |
| GTTGATGACT TCAAGGGACG GTTGTCTTC TCTCTAGACT CCTCTGTCAG CACGGCATAT  | 120 |
| CTACAGATCA GCAG   | 134 |

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

GGTACCCTGG CCCAGTAAG TAAAAGGGAA GTAACCATCC ATATTCCTT CTCTCGTACA      60
GTAATACACT GCAGTGTCTG CAGCCTTTAG GCTGCTGATC TGTAGATATG CCGTGCTGAC    120
AGAGGAGTCT AGAG                                     134

```

## (2) INFORMATION FOR SEQ ID NO:47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...225
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

CCT GGA CAA GGG CTC AAG TGG ATG GGA TGG ATA AAC ACC AGA AAT GGA      48
Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr Arg Asn Gly
  1              5              10              15

AAG TCA ACA TAT GTT GAT GAC TTC AAG GGA CGG TTT GTC TTC TCT CTA      96
Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Val Phe Ser Leu
    20              25              30

GAC TCC TCT GTC AGC ACG GCA TAT CTA CAG ATC AGC AGC CTA AAG GCT      144
Asp Ser Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala
    35              40              45

```

GAC GAC ACT GCA GTG TAT TAC TGT ACG AGA GAA GGG AAT ATG GAT GGT 192  
 Asp Asp Thr Ala Val Tyr Tyr Cys Thr Arg Glu Gly Asn Met Asp Gly  
 50 55 60

TAC TTC CCT TTT ACT TAC TGG GGC CAG GGT ACC 225  
 Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr  
 65 70 75

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr Arg Asn Gly  
 1 5 10 15  
 Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Val Phe Ser Leu  
 20 25 30  
 Asp Ser Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala  
 35 40 45  
 Asp Asp Thr Ala Val Tyr Tyr Cys Thr Arg Glu Gly Asn Met Asp Gly  
 50 55 60  
 Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr  
 65 70 75

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCCTGGAC AAGGGCTCAA GTGGATG

27

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TTTGGTACCC TGGCCCCAGT AAGT

24

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...363  
(D) OTHER INFORMATION: F9HZHC 1-1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CAG | GTG | CAA | CTA | GTG | CAA | TCT | GGG | TCT | GAG | TTG | AAG | AAG | CCT | GGG | GCC | 48  |
| Gln | Val | Gln | Leu | Val | Gln | Ser | Gly | Ser | Glu | Leu | Lys | Lys | Pro | Gly | Ala |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| TCA | GTG | AAG | GTT | TCC | TGC | AAG | GCC | TCT | GGA | TAC | ACC | TTC | ACT | AAC | TAT | 96  |
| Ser | Val | Lys | Val | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Thr | Asn | Tyr |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GGA | ATG | AAC | TGG | GTG | CGA | CAG | GCC | CCT | GGA | CAA | GGG | CTC | AAG | TGG | ATG | 144 |
| Gly | Met | Asn | Trp | Val | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu | Lys | Trp | Met |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| GGA | TGG | ATA | AAC | ACC | AGA | AAT | GGA | AAG | TCA | ACA | TAT | GTT | GAT | GAC | TTC | 192 |
| Gly | Trp | Ile | Asn | Thr | Arg | Asn | Gly | Lys | Ser | Thr | Tyr | Val | Asp | Asp | Phe |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| AAG | GGA | CGG | TTT | GTC | TTC | TCT | CTA | GAC | TCC | TCT | GTC | AGC | ACG | GCA | TAT | 240 |
| Lys | Gly | Arg | Phe | Val | Phe | Ser | Leu | Asp | Ser | Ser | Val | Ser | Thr | Ala | Tyr |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| CTA | CAG | ATC | AGC | AGC | CTA | AAG | GCT | GAC | GAC | ACT | GCA | GTG | TAT | TAC | TGT | 288 |
| Leu | Gln | Ile | Ser | Ser | Leu | Lys | Ala | Asp | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| ACG | AGA | GAA | GGG | AAT | ATG | GAT | GGT | TAC | TTC | CCT | TTT | ACT | TAC | TGG | GGC | 336 |
| Thr | Arg | Glu | Gly | Asn | Met | Asp | Gly | Tyr | Phe | Pro | Phe | Thr | Tyr | Trp | Gly |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| CAG | GGT | ACC | CTG | GTC | ACC | GTC | TCC | TCA |     |     |     |     |     |     |     | 363 |
| Gln | Gly | Thr | Leu | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |     |



## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
 1             5             10             15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
      20             25             30
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Lys Trp Met
      35             40             45
Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe
      50             55             60
Lys Gly Arg Phe Val Phe Ser Leu Asp Ser Ser Val Ser Thr Ala Tyr
      65             70             75             80
Leu Gln Ile Ser Ser Leu Lys Ala Asp Asp Thr Ala Val Tyr Tyr Cys
      85             90             95
Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly
      100            105            110
Gln Gly Thr Leu Val Thr Val Ser Ser
      115            120

```

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

|   |    |
|---|----|
| CAACAGAGAC CTGGCCAGGC TCCCAAGCCC TGGATCTATG CCACGAGTAA CCTGGCTAGC | 60 |
| GGCGTCCCAG CCAGGTTTCAG TG   | 82 |

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 90 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

|   |    |
|---|----|
| GATCCACTGA ACCTGGCTGG GACGCCGCTA GCCAGGTTAC TCGTGGCATA GATCCAGGGC | 60 |
| TTGGGAGCCT GGCCAGGTCT CTGTTGGTAC                                  | 90 |

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gln | Arg | Pro | Gly | Gln | Ala | Pro | Lys | Pro | Trp | Ile | Tyr | Ala | Thr | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asn | Leu | Ala | Ser | Gly | Val | Pro | Ala | Arg | Phe | Ser |     |     |     |     |     |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...321

(D) OTHER INFORMATION: F9HZLC 1-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GAA | ATA | GTA | CTG | ACA | CAG | TCT | CCA | GCC | ACC | CTG | TCT | TTG | TCT | CCA | GGG | 48  |
| Glu | Ile | Val | Leu | Thr | Gln | Ser | Pro | Ala | Thr | Leu | Ser | Leu | Ser | Pro | Gly |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| GAA | AGA | GCC | ACC | CTC | TCC | TGC | AGG | GCC | AGC | TCA | AGT | GTA | AAT | TAC | ATG | 96  |
| Glu | Arg | Ala | Thr | Leu | Ser | Cys | Arg | Ala | Ser | Ser | Ser | Val | Asn | Tyr | Met |     |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| CAC | TGG | TAC | CAA | CAG | AGA | CCT | GGC | CAG | GCT | CCC | AAG | CCC | TGG | ATC | TAT | 144 |
| His | Trp | Tyr | Gln | Gln | Arg | Pro | Gly | Gln | Ala | Pro | Lys | Pro | Trp | Ile | Tyr |     |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

GCC ACG AGT AAC CTG GCT AGC GGC GTC CCA GCC AGG TTC AGT GGA TCC 192  
 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser  
           50                          55                          60

GGG TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTA GAG CCT GAA 240  
 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu  
           65                          70                          75                          80

GAT TTT GCG GTT TAT TAC TGT CAG CAG TGG AGT ATT AAC CCG CGG ACG 288  
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr  
                                   85                          90                          95

TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA 321  
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
                           100                          105

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
       1                          5                          10                          15  
 His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr  
           35                          40                          45  
 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser  
           50                          55                          60  
 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu  
       65                          70                          75                          80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr  
                             85                            90                            95  
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
                             100                            105

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GATCCGGGTC TGGGACAGAT TACACTCTCA CGATATCCAG T

41

## (2) INFORMATION FOR SEQ ID NO:59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CTAGACTGGA TATCGTGAGA GTGTAATCTG TCCCAGACCC G

41

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE: internal

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

## (A) NAME/KEY: Coding Sequence

## (B) LOCATION: 1...321

## (D) OTHER INFORMATION: F9HZLC 1-2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

|   |     |
|---|-----|
| GAA ATA GTA CTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG | 48  |
| Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly |     |
| 1 5 10 15   |     |
| GAA AGA GCC ACC CTC TCC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG | 96  |
| Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Asn Tyr Met |     |
| 20 25 30  |     |
| CAC TGG TAC CAA CAG AGA CCT GGC CAG GCT CCC AAG CCC TGG ATC TAT | 144 |
| His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr |     |
| 35 40 45  |     |
| GCC ACG AGT AAC CTG GCT AGC GGC GTC CCA GCC AGG TTC AGT GGA TCC | 192 |
| Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser |     |
| 50 55 60  |     |
| GGG TCT GGG ACA GAT TAC ACT CTC ACG ATA TCC AGT CTA GAG CCT GAA | 240 |
| Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu |     |
| 65 70 75 80   |     |
| GAT TTT GCG GTT TAT TAC TGT CAG CAG TGG AGT ATT AAC CCG CGG ACG | 288 |
| Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr |     |
| 85 90 95  |     |
| TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA                     | 321 |
| Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg                     |     |
| 100 105   |     |

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ile | Val | Leu | Thr | Gln | Ser | Pro | Ala | Thr | Leu | Ser | Leu | Ser | Pro | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Arg | Ala | Thr | Leu | Ser | Cys | Arg | Ala | Ser | Ser | Ser | Val | Asn | Tyr | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Trp | Tyr | Gln | Gln | Arg | Pro | Gly | Gln | Ala | Pro | Lys | Pro | Trp | Ile | Tyr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Thr | Ser | Asn | Leu | Ala | Ser | Gly | Val | Pro | Ala | Arg | Phe | Ser | Gly | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ser | Gly | Thr | Asp | Tyr | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Glu | Pro | Glu |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Phe | Ala | Val | Tyr | Tyr | Cys | Gln | Gln | Trp | Ser | Ile | Asn | Pro | Arg | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Gly | Gly | Gly | Thr | Lys | Val | Glu | Ile | Lys | Arg |     |     |     |     |     |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| AGTACTCACC | CAGAGCCCAA | GCAGCCTGAG | CGCCAGCGTG | GGTGACAGAG | TGACCATCAC | 60  |
| CTGCAGGGCC | AGCTCAAGTG | TAAATTACAT | GCACTGGTAC | CAGCAGAAGC | CAGGTAAGGC | 120 |
| TCCAAAGCCT | TGGATCTACG | CCACTAGTAA | CCTGGCTTCT | GGTGT      |            | 165 |



## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

CCGCGGGTTA ATACTCCACT GCTGGCAGTA GTAGGTGGCG ATATCCTCTG GCTGGAGGCT      60
GCTGATGGTG AAGGTGTAGT CTGTACCGCT ACCGGATCCG CTGAATCTGC TTGGCACACC    120
AGAAGCCAGG TTACTAGTGG CGTAGATCCA AGGCTTTGGA G                          161

```

## (2) INFORMATION FOR SEQ ID NO:65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 2...280

(D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

A GTA CTC ACC CAG AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT GAC AGA 49  
 Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
 1 5 10 15  
  
 GTG ACC ATC ACC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG CAC TGG 97  
 Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met His Trp  
 20 25 30  
  
 TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG CCT TGG ATC TAC GCC ACT 145  
 Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Ala Thr  
 35 40 45  
  
 AGT AAC CTG GCT TCT GGT GTG CCA AGC AGA TTC AGC GGA TCC GGT AGC 193  
 Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser  
 50 55 60  
  
 GGT ACA GAC TAC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAT ATC 241  
 Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile  
 65 70 75 80  
  
 GCC ACC TAC TAC TGC CAG CAG TGG AGT ATT AAC CCG CGG 280  
 Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg  
 85 90

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1              5              10              15
Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met His Trp
      20              25              30
Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Ala Thr
      35              40              45
Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
      50              55              60
Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile
65              70              75              80
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg
      85              90

```

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TTTAGTACTC ACCCAGAGCC CAAGCAG

27

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TTCCGCGGGT TAATACTCCA CTGCTGG

27

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTCGAGCAGT ACTATCTGGG AGTGGACACC TGT

33

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile | Lys | Arg | Thr | Val | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGACGTTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGGAC TGTGGCGG

48

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CGCCGCCACA GTCCGTTTGA TTTCCACCTT GGTCCCTTGG CCGAACGTCC GC

52

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...321  
(D) OTHER INFORMATION: F9HZLC 2-0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

107

GAT ATC GCC ACC TAC TAC TGC CAG CAG TGG AGT ATT AAC CCG CGG ACG 288  
 Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr  
                   85                  90                  95

TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGG 321  
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg  
                   100                  105

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gln Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
   1                  5                  10                  15  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met  
                   20                  25                  30  
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr  
                   35                  40                  45  
 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
                   50                  55                  60  
 Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu  
   65                  70                  75                  80  
 Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr  
                   85                  90                  95  
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg  
                   100                  105

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 27...94

(D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

|  |    |
|--|----|
| GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC | 53 |
| Met Gly Trp Ser Cys Ile Ile Leu Phe                              |    |
| 1 5  |    |

|   |    |
|---|----|
| TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG ATA GTA CT  | 94 |
| Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Ile Val Leu |    |
| 10 15 20  |    |

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO



(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1           5           10           15
Val His Ser Gln Ile Val Leu
                20

```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 27...401
- (D) OTHER INFORMATION: F9HZLC 1-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC      53
                Met Gly Trp Ser Cys Ile Ile Leu Phe
                1           5

TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG ATA GTA CTG ACA CAG      101
Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Ile Val Leu Thr Gln
10           15           20           25

```

|   |     |
|---|-----|
| TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC | 149 |
| Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser |     |
| 30 35 40  |     |
| TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG CAC TGG TAC CAA CAG AGA | 197 |
| Cys Arg Ala Ser Ser Ser Val Asn Tyr Met His Trp Tyr Gln Gln Arg |     |
| 45 50 55  |     |
| CCT GGC CAG GCT CCC AAG CCC TGG ATC TAT GCC ACG AGT AAC CTG GCT | 245 |
| Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala |     |
| 60 65 70  |     |
| AGC GGC GTC CCA GCC AGG TTC AGT GGA TCC GGG TCT GGG ACA GAT TAC | 293 |
| Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr |     |
| 75 80 85  |     |
| ACT CTC ACG ATA TCC AGT CTA GAG CCT GAA GAT TTT GCG GTT TAT TAC | 341 |
| Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr |     |
| 90 95 100 105   |     |
| TGT CAG CAG TGG AGT ATT AAC CCG CGG ACG TTC GGC GGA GGG ACC AAG | 389 |
| Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr Phe Gly Gly Gly Thr Lys |     |
| 110 115 120   |     |
| GTG GAG ATC AAA   | 401 |
| Val Glu Ile Lys   |     |
| 125   |     |

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE: internal

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1           5           10           15
Val His Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu
          20           25           30
Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val
          35           40           45
Asn Tyr Met His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Lys Pro
          50           55           60
Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe
65           70           75           80
Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu
          85           90           95
Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn
          100          105          110
Pro Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          115          120          125

```

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

AGGCCTCTGG ATACACCTTC ACTAACTATG GAATGAACTG GGTGCGACAG GCCCCTGGAC 60
AAGGGCTCGA GTGGATGGGA T                                     81

```

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

|   |    |
|---|----|
| TGTCTAGAGA GAAGACAAAC CGTCCCTTGA AGTCATCAAC ATATGTTGAC TTTCCATTTC | 60 |
| TGGTGTTTAT CCATCCCATC CACTCGAGCC CTTGTCCAG                        | 99 |

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

|   |    |
|---|----|
| GGTTTGTCTT CTCTCTAGAC ACCTCTGTCA GCACGGCATA TCTACAGATC AGCAGCCTAA | 60 |
| AGGCTGAGGA CACTGCAGTG TATTTCT                                     | 87 |

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

GGTACCCTGG CCCCAGTAAG TAAAAGGGAA GTAACCATCC ATATTCCCTT CTCTCGTACA 60  
GAAATACACT GCAGTGTCTT CAGCCT 86

```

AAT GGA AAG TCA ACA TAT GTT GAT GAC TTC AAG GGA CGG TTT GTC TTC      143
Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Val Phe
      35              40              45

TCT CTA GAC ACC TCT GTC AGC ACG GCA TAT CTA CAG ATC AGC AGC CTA      191
Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu
      50              55              60

AAG GCT GAG GAC ACT GCA GTG TAT TTC TGT ACG AGA GAA GGG AAT ATG      239
Lys Ala Glu Asp Thr Ala Val Tyr Phe Cys Thr Arg Glu Gly Asn Met
      65              70              75

GAT GGT TAC TTC CCT TTT ACT TAC TGG GGC CAG GGT ACC      278
Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr
      80              85              90

```

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE: internal

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln
 1              5              10              15
Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Arg Asn
      20              25              30
Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Val Phe Ser
      35              40              45
Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys
      50              55              60
Ala Glu Asp Thr Ala Val Tyr Phe Cys Thr Arg Glu Gly Asn Met Asp
65              70              75              80

```

Gly Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr  
 85 90

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

AGGCCTCTGG ATACACCTTC ACTAACTATG

30

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGTACCCTGG CCCAGTAAG TAAAAG

26

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CCAGACTCGA CTAGTTGGAT CTGGGAGTGG ACACCTG

37

## (2) INFORMATION FOR SEQ ID NO:88:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 27...446

(D) OTHER INFORMATION: F9HZHC 3-0



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

|  |     |
|--|-----|
| GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC | 53  |
| Met Gly Trp Ser Cys Ile Ile Leu Phe                              |     |
| 1 5  |     |
| TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG ATC CAA CTA GTG CAA  | 101 |
| Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Ile Gln Leu Val Gln  |     |
| 10 15 20 25  |     |
| TCT GGG TCT GAG TTG AAG AAG CCT GGG GCC TCA GTG AAG GTT TCC TGC  | 149 |
| Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys  |     |
| 30 35 40   |     |
| AAG GCC TCT GGA TAC ACC TTC ACT AAC TAT GGA ATG AAC TGG GTG CGA  | 197 |
| Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Arg  |     |
| 45 50 55   |     |
| CAG GCC CCT GGA CAA GGG CTC GAG TGG ATG GGA TGG ATA AAC ACC AGA  | 245 |
| Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Arg  |     |
| 60 65 70   |     |
| AAT GGA AAG TCA ACA TAT GTT GAT GAC TTC AAG GGA CGG TTT GTC TTC  | 293 |
| Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Val Phe  |     |
| 75 80 85   |     |
| TCT CTA GAC ACC TCT GTC AGC ACG GCA TAT CTA CAG ATC AGC AGC CTA  | 341 |
| Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu  |     |
| 90 95 100 105  |     |
| AAG GCT GAG GAC ACT GCA GTG TAT TTC TGT ACG AGA GAA GGG AAT ATG  | 389 |
| Lys Ala Glu Asp Thr Ala Val Tyr Phe Cys Thr Arg Glu Gly Asn Met  |     |
| 110 115 120  |     |
| GAT GGT TAC TTC CCT TTT ACT TAC TGG GGC CAG GGT ACC CTG GTC ACC  | 437 |
| Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr  |     |
| 125 130 135  |     |
| GTC TCC TCT  | 446 |
| Val Ser Ser  |     |
| 140  |     |

## (2) INFORMATION FOR SEQ ID NO:89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1             5             10             15
Val His Ser Gln Ile Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys
          20             25             30
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
          35             40             45
Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
          50             55             60
Glu Trp Met Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val
65             70             75             80
Asp Asp Phe Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser
          85             90             95
Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val
          100            105            110
Tyr Phe Cys Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr
          115            120            125
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
          130            135            140

```

## (2) INFORMATION FOR SEQ ID NO:90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

|   |    |
|---|----|
| AGTACTGACA CAGTCTCCAT CCTCCCTGTC TGCATCTGTT GGGGACAGAG TCACCATCAC | 60 |
| TTGCAGGGCC AGCTCAAGTG TAAATTACAT                                  | 90 |

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

|   |     |
|---|-----|
| CTTGATGGGA CGCCGCTAGC CAGGTTACTC GTGGCATAGA TCCAGGGCTT GGGAGCTTTG | 60  |
| CCAGGTTTCT GTTGGTACCA GTGCATGTAA TTTACACTTG AGCTGGCC              | 108 |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

|   |     |
|---|-----|
| TAACCTGGCT AGCGGCGTCC CATCAAGGTT CAGTGGATCC GGGTCTGGGA CAGATTACAC | 60  |
| TCTCACGATA TCCAGTCTAC AACCTGAAGA TTTTGC GACT TATTACTG             | 108 |

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

|   |     |
|---|-----|
| GGCGCCGCCA CAGTTCGTTT GATCTCCAGC TTGGTCCCTC CGCCGAACGT CCGCGGGTTA | 60  |
| ATACTCCACT GCTGACAGTA ATAAGTCGCA AAATCTTCAG GT                    | 102 |

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 2...328  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| A   | GTA | CTG | ACA | CAG | TCT | CCA | TCC | TCC | CTG | TCT | GCA | TCT | GTT | GGG | GAC | AGA | 49  |
|     | Val | Leu | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly | Asp | Arg |     |
|     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GTC | ACC | ATC | ACT | TGC | AGG | GCC | AGC | TCA | AGT | GTA | AAT | TAC | ATG | CAC | TGG |     | 97  |
| Val | Thr | Ile | Thr | Cys | Arg | Ala | Ser | Ser | Ser | Val | Asn | Tyr | Met | His | Trp |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| TAC | CAA | CAG | AAA | CCT | GGC | AAA | GCT | CCC | AAG | CCC | TGG | ATC | TAT | GCC | ACG |     | 145 |
| Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Pro | Trp | Ile | Tyr | Ala | Thr |     |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| AGT | AAC | CTG | GCT | AGC | GGC | GTC | CCA | TCA | AGG | TTC | AGT | GGA | TCC | GGG | TCT |     | 193 |
| Ser | Asn | Leu | Ala | Ser | Gly | Val | Pro | Ser | Arg | Phe | Ser | Gly | Ser | Gly | Ser |     |     |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GGG | ACA | GAT | TAC | ACT | CTC | ACG | ATA | TCC | AGT | CTA | CAA | CCT | GAA | GAT | TTT |     | 241 |
| Gly | Thr | Asp | Tyr | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Pro | Glu | Asp | Phe |     |     |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GCG | ACT | TAT | TAC | TGT | CAG | CAG | TGG | AGT | ATT | AAC | CCG | CGG | ACG | TTC | GGC |     | 289 |
| Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Trp | Ser | Ile | Asn | Pro | Arg | Thr | Phe | Gly |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GGA | GGG | ACC | AAG | CTG | GAG | ATC | AAA | CGA | ACT | GTG | GCG | GCG | CC  |     |     |     | 330 |
| Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Thr | Val | Ala | Ala |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```

Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1             5             10             15
Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met His Trp
          20             25             30
Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Ala Thr
          35             40             45
Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
          50             55             60
Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
65             70             75             80
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr Phe Gly
          85             90             95
Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
          100             105

```

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CAAGTACTGA CACAGTCTCC ATCCTC

26

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AGGGCGCCGC CACAGTTCGT TTGATC

26

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 27...412

(D) OTHER INFORMATION: F9HZLC 3-0

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

|  |     |
|--|-----|
| GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC | 53  |
| Met Gly Trp Ser Cys Ile Ile Leu Phe                              |     |
| 1 5  |     |
| TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG ATA GTA CTG ACA CAG  | 101 |
| Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Ile Val Leu Thr Gln  |     |
| 10 15 20 25  |     |
| TCT CCA TCC TCC CTG TCT GCA TCT GTT GGG GAC AGA GTC ACC ATC ACT  | 149 |
| Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr  |     |
| 30 35 40   |     |
| TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG CAC TGG TAC CAA CAG AAA  | 197 |
| Cys Arg Ala Ser Ser Ser Val Asn Tyr Met His Trp Tyr Gln Gln Lys  |     |
| 45 50 55   |     |
| CCT GGC AAA GCT CCC AAG CCC TGG ATC TAT GCC ACG AGT AAC CTG GCT  | 245 |
| Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala  |     |
| 60 65 70   |     |
| AGC GGC GTC CCA TCA AGG TTC AGT GGA TCC GGG TCT GGG ACA GAT TAC  | 293 |
| Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr  |     |
| 75 80 85   |     |
| ACT CTC ACG ATA TCC AGT CTA CAA CCT GAA GAT TTT GCG ACT TAT TAC  | 341 |
| Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr  |     |
| 90 95 100 105  |     |
| TGT CAG CAG TGG AGT ATT AAC CCG CGG ACG TTC GGC GGA GGG ACC AAG  | 389 |
| Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr Phe Gly Gly Gly Thr Lys  |     |
| 110 115 120  |     |
| CTG GAG ATC AAA CGA ACT GTG GC                                   | 412 |
| Leu Glu Ile Lys Arg Thr Val Val                                  |     |
| 125  |     |



## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1             5             10             15
Val His Ser Gln Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
          20             25             30
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val
          35             40             45
Asn Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro
          50             55             60
Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe
65             70             75             80
Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu
          85             90             95
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn
          100            105            110
Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
          115            120            125
Val

```

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CAAATAGTAC TCTCCCAGTC TCCAGC

26

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 41 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGATAAGCTT GGCGCCGCAA CAGTCGGTTT GATTTCAGC T

41

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 335 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...335  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

|   |     |
|---|-----|
| CAG ATA GTA CTC TCC CAG TCT CCA GCA ATC CTG TCT GCA TCT CCA GGG | 48  |
| Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly |     |
| 1 5 10 15   |     |
| GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG | 96  |
| Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met |     |
| 20 25 30  |     |
| CAC TGG TAC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG ATT TAT | 144 |
| His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr |     |
| 35 40 45  |     |
| GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT GCT CGC TTC AGT GGC AGT | 192 |
| Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser |     |
| 50 55 60  |     |
| GGG TCT GGG ACC TCT TAC TCT CTC ACA ATC AGC AGA GTG GAG GCT GAA | 240 |
| Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu |     |
| 65 70 75 80   |     |
| GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG AGT ATT AAC CCA CGG ACG | 288 |
| Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr |     |
| 85 90 95  |     |
| TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGG ACT GTT GCG GCG CC  | 335 |
| Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro |     |
| 100 105 110   |     |

## (2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

```
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: internal
(vi) ORIGINAL SOURCE:
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ile | Val | Leu | Ser | Gln | Ser | Pro | Ala | Ile | Leu | Ser | Ala | Ser | Pro | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Lys | Val | Thr | Met | Thr | Cys | Arg | Ala | Ser | Ser | Ser | Val | Asn | Tyr | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Ser | Ser | Pro | Lys | Pro | Trp | Ile | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Thr | Ser | Asn | Leu | Ala | Ser | Gly | Val | Pro | Ala | Arg | Phe | Ser | Gly | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ser | Gly | Thr | Ser | Tyr | Ser | Leu | Thr | Ile | Ser | Arg | Val | Glu | Ala | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Ala | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Trp | Ser | Ile | Asn | Pro | Arg | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Gly | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Thr | Val | Ala | Ala | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

(2) INFORMATION FOR SEQ ID NO:105:

(A) LENGTH: 106 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

130

(iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE: internal  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ile | Val | Leu | Ser | Gln | Ser | Pro | Ala | Ile | Leu | Ser | Ala | Ser | Pro | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Lys | Val | Thr | Met | Thr | Cys | Arg | Ala | Ser | Ser | Ser | Val | Asn | Tyr | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Ser | Ser | Pro | Lys | Pro | Trp | Ile | Tyr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Thr | Ser | Asn | Leu | Ala | Ser | Gly | Val | Pro | Ala | Arg | Phe | Ser | Gly | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ser | Gly | Thr | Ser | Tyr | Ser | Leu | Thr | Ile | Ser | Arg | Val | Glu | Ala | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Ala | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Trp | Ser | Ile | Asn | Pro | Arg | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Gly | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys |     |     |     |     |     |     |
|     |     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CAGATCCAAC TAGTGCAGTC TGGACCTGAG

30

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TTAAGCTTGC TAGCTGCAGA GACAGTGACC AG

32

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...369

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

[illegible]

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE: internal  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1             5             10             15
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
      20             25             30
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
      35             40             45
Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe
      50             55             60
Lys Gly Arg Phe Ala Phe Ser Leu Glu Ser Ser Ala Ser Thr Ala Asn
      65             70             75             80
Leu Gln Ile Asp Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys
      85             90             95
Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly
      100            105            110
Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser
      115            120

```

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

(2) INFORMATION FOR SEQ ID NO:111:

(A) LENGTH: 121 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ile | Gln | Leu | Val | Gln | Ser | Gly | Pro | Glu | Leu | Lys | Lys | Pro | Gly | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Val | Lys | Ile | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Thr | Asn | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Gly | Met | Asn | Trp | Val | Lys | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Lys | Trp | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Gly | Trp | Ile | Asn | Thr | Arg | Asn | Gly | Lys | Ser | Thr | Tyr | Val | Asp | Asp | Phe |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Gly | Arg | Phe | Ala | Phe | Ser | Leu | Glu | Ser | Ser | Ala | Ser | Thr | Ala | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Gln | Ile | Asp | Asn | Leu | Lys | Asp | Glu | Asp | Thr | Ala | Thr | Tyr | Phe | Cys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Arg | Glu | Gly | Asn | Met | Asp | Gly | Tyr | Phe | Pro | Phe | Thr | Tyr | Trp | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Gln | Gly | Thr | Leu | Val | Thr | Val | Ser | Ala |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |